SEQUENCE LISTING

<110> Arthur Scherf Louis H. Miller Benoit Gamain Dror I. Baruch Pierre Buffet Christine Scheidig Jurg Gysin Bruno Pouvelle Nobutaka Fujii Joseph Smith

<120> IDENTIFICATION OF THE DOMAIN OF PLASMODIUM FALCIPARUM ERYTHROCYTE MEMBRANE PROTEIN 1 (PFEMP1) THAT MEDIATES ADHESION TO CHONDROITIN SULFATE A

<130> NIH176.001C1

<150> PCT/US00/24195

<151> 2000-09-01

<150> 60/152,023

<151> 1999-09-01

<160> 11

<170> FastSEQ for Windows Version 4.0

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<212> DNA

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Gln Ser Gln Val Asn Leu Lys Glu Ala Phe lle Lys Ser Ala Ala Ala 1330 1335 1340
Glu Thr Phe Phe Ser Trp Tyr Tyr Tyr Lys Ser Lys Asp Gly Glu Gly 1345 1350 1355 1360
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Gly Thr Asp Ile Ser Lys Gly His Gly Glu Gly Ser Lys Leu Lys Glu 1395 1400 1405
Gin lie Asp Ser Leu Phe Lys Asn Gly Asp Gln Lys Ser Pro Asn Gly 1410 1415 1420
Lys Thr Arg Gln Glu Trp Trp Thr Glu His Ser His Glu Ile Trp Glu 1425 1430 1435 1440
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Thr Glu Asn Tyr Gly Tyr Asn Asn Val Lys Phe Ser Asp Lys Ser Thr 1460 1465 1470
Thr Leu Glu Glu Phe Ala Lys Arg Pro Gln Phe Leu Arg Trp Leu Thr 1475 1480 1485
Glu Trp Tyr Asp Asp Tyr Cys Tyr Thr Arg Gln Lys Tyr Leu Lys Asp 1490 1495 1500
Val Gln Glu Lys Cys Lys Ser Asn Asp Gln Leu Lys Cys Asp Thr Glu 1505 1510 1515 1520
Cys Asn Lys Lys Cys Glu Asp Tyr Val Lys Tyr Met Lys Lys Lys 1525 1530 1535
Glu Trp lle Pro Gln Asp Lys Tyr Tyr Lys Asp Glu Arg Asp Lys Lys 1540 1545 1550
Arg Phe Asp Arg Gln His Ile Gly Val Met Val Thr Asp Tyr Thr Gly 1555 1560 1565
Thr Asn Ala Thr Asp Tyr Leu Asn Arg Lys Phe Thr Ala Ser Cys Gly 1570 1575 1580
Asp Lys Pro Gly Ser Ala Ser Val Val Gln Arg Asn Ile Gln Leu Leu 1585 1590 1595 1600
Glu Lys Gln Ala Tyr Tyr Asp Ala Asp Lys His Cys Gly Cys Thr Lys 1605 1610 1615
Phe Ile Glu Asn Asp Asp Lys Tyr Thr Asn Ile Ser Ser Lys Asp Lys 1620 1625 1630
Cys Lys Gly Leu Val Lys Glu Ala Asn Thr Gly Ala Ile Lys Trp Gln 1635 1640 1645
Asn Lys Gly Pro Asn Asn Tyr Asn Asn Leu Lys Glu Leu Thr Glu Asp 1650 1655 1660
Val Leu Phe Pro Ser Arg Arg Leu Arg Ile Cys Phe His Ala Leu Asp 1665 1670 1675 1680
Gly Asn Tyr Thr Asp Pro Glu Val Lys Asp Glu Asn Gly Leu Arg Lys 1685 1690 1695
Arg Leu Met Glu Val Ala Ala Thr Glu Gly Tyr Asn Leu Gly Gln Tyr 1700 1705 1710
Tyr Lys Glu Lys Glu Lys Glu Lys Ile Lys Thr Ser Asp Ala His 1715 1720 1725

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3.80
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2165 2170 2175
Asn Pro Ala Ala Glu Asn Glu Leu Gln Asn Gly Thr Ile Pro Asp Glu 2180 2185 2190
Phe Lys Arg IIe Met Tyr Tyr Thr Tyr Gly Asp Tyr Lys Asp Met Phe 2195 2200 2205
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Ser Val Thr Thr Ile Leu Asn Glu Asn Asn Lys Lys Gln Asp Lys 2225 2230 2235 2240
Lys Lys Asp Glu Glu Leu Arg Lys Ile Phe Trp Glu Lys Asn Lys Lys 2245 2250 2255
Phe Ile Trp Glu Gly Met Ile Tyr Gly Leu Thr Tyr His Leu Thr Asp 2260 2265 2270
Glu Asn Glu Lys Glu Lys Ile Arg Asp Asn Tyr Gln Tyr Asn Asp Met 2275 2280 2285
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Gly Ser Asn Asp Gly Lys Thr Gln Glu Cys Ala Glu Ala Cys Val Thr 2340 2345 2350
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Glu Lys Phe Lys Lys Asp Lys Asp Gly Lys Lys Tyr Lys Asp Tyr Pro 2370 2375 2380
Ser Thr Glu Arg Asp Ile Glu Lys Ala Thr Cys Ala His Glu Tyr Leu 2385 2390 2395 2400
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Gln Lys Pro Ser Ser Gln Leu Pro Lys Thr Thr Gln Gln Ser Gln Ser 2420 2425 2430
Ser Asp Ala Asn Asp Met Pro Glu Ser Leu Asp Tyr Val Pro Glu Glu 2435 2440 2445
Phe Asn Lys Cys Glu Cys Pro Glu Leu Ser Lys Lys Gly Ser Met IIe 2450 2455 2460
His Thr Lys Lys Ile Thr Glu Pro Lys Ile Pro Met Asn Cys Val Glu 2465 2470 2475 2480
Lys Ala Ala Tyr Tyr Leu Ser Lys Glu Ala Glu Asn Asn Met Asp Ile 2485 2490 2495
Thr Leu Lys Glu Lys Phe lle Pro lle Glu Ser Thr Lys Glu Lys Glu 2500 2510
Ser Lys Asn Ser Trp Thr Asn Asn Asn Pro Cys Asp Pro Lys Lys Pro 2515 2520 2525
Tyr Ala Pro Asp Lys Tyr Ile Gly Arg Arg Asn Pro Cys Glu Asn Arg 2530 2535 2540
Glu Glu Asn Arg Phe Lys Val Asp Tyr Glu Trp Lys Cys Tyr Lys Asn 2545 2550 2555 2560
Ser Lys Phe Tyr Gln Glu Lys Lys Arg Val Cys Val Pro Pro Arg Arg 2565 2570 2575
Glu His Met Cys Leu Arg Asn Leu Asp Glu Ile Lys Ile Glu Arg Leu 2580 2585 2590
Lys Asp Ser Asn Tyr Leu Leu Lys Met Val Arg Arg Thr Ala Arg Asn 2595 2600 2605

	2610 2615 2620
	2610 2615 2620
Ė	Met Asn Pro Ile Cys Asp Thr Met Lys Tyr Ser Phe Ala Asp Leu Gly
	2625 2630 2635 2640
	Asp Ile Val Arg Gly Thr Asp Met Leu Arg Ile Gly Gly Tyr Leu Pro 2645 2650 2655
	Pro Val Glu lle Lys Leu Tyr Lys Val Phe Glu Tyr lle Tyr Gly Lys
	2660 2665 2670
	Trp Arg Asn Lys Asn Lys Gly Arg Asn Lys Tyr Asn Asp Val Gln Thr
	Phe Arg Ser Ala Trp Trp Asp Ala Asn Arg Lys Asp Ile Trp Lys Ala
	Met Thr Cys Lys Ala Pro Glu Asp Ala Lys Leu Phe Arg Lys Gly Arg
	2705 2710 2/15 2/20 Met Asp Gly Phe Glu Arg Ile Thr Leu Ile Gln Asp Lys Cys Gly His
	2725 2730 2735
	Lys Asp Asp Pro Pro Val Asp Asp Tyr lle Pro Gln Arg Phe Arg Trp 2740 2745 2750
	Met Thr Glu Trp Ser Glu Tyr Tyr Cys Lys Ala Leu Met Glu Glu Leu 2755 2760 2765
	Glu Lys Phe Lys Lys Ser Cys Asp His Cys Lys Thr Ser Asp Arg Cys
£ a	2770 2775 2780 Lys Asn Asp Tyr Asp Glu Asn Lys Cys Glu Gln Cys Lys Thr Arg Cys
Serie Serie	2785 2790 2795 2800
100	Gin Glu Tyr Lys Asn Phe Val Leu Lys Trp Lys Ser Leu Phe Asp Ile
22	2805 2810 2815
	Gin Ser Asn Lys Tyr Lys Glu Leu Tyr Glu Gin Pro lle Tyr Thr Lys 2820 2825 2830
in the second	lle Ser Thr Tyr Asp His Val Gln Asn Phe Val Gln Lys Leu Lys Thr
i d	2835 2840 2845
	Phe Lys Ser Glu Cys Ser Val Glu Ser Phe Ser Glu Tyr Leu His Glu
8	2850 2855 2860
	Thr Ser Lys Cys Leu Asn Tyr Lys Phe Asn Glu Asn Asp Gly Ser Ser
Ting.	2865 2870 2875 2880
	Asn Ile Arg Thr Tyr Ala Phe Glu Glu Thr Pro Lys Ser Tyr Lys Glu 2885 2890 2895
£24.	Ala Cys Ser Cys Thr Leu Pro Ser Lys Asn Pro Leu Asp Asn Cys Pro
	2900 2905 2910
± 412	Thr Asp Gln Asn Lys Asp Gly Cys Lys Glu Leu Gln Thr Phe Thr Phe
	2915 2920 2925
	Cys Ser Lys Asn Asp Tyr Asp Asn Asn Leu Asp Asn Trp Asn Ala Ty
	2930 2935 2940
	Leu Val Leu Asn Ser Ser Asp Asp Asn Lys Gly Val Leu Ile Pro Pro 2945 2950 2955 2960
	2945 2950 2955 2960 Arg Arg Arg His Leu Cys Thr Arg Pro Ile Thr Ala Tyr Asn Tyr Arg
	2965 2970 2975
	Lys Gly Asp Lys Glu lie Leu Lys Lys Lys Leu Leu Thr Ser Ala Phe
	2980 2985 2990
	Ser Gin Gly Gin Leu Leu Gly Gin Lys Tyr Lys Ser Glu Glu Glu Leu
	2995 3000 3005
	Cys Phe Glu Ala Met Lys Tyr Ser Tyr Ala Asp Tyr Ser Asp Ile Ile 3010 3015 3020
	3010 3015 3020 Lys Gly Thr Asp Met Met Asp Thr Ser Leu Ser Glu Lys Ile Lys Lys
	0005 0040
	3025 3030 3035 3040 Ile Phe Glu Thr Ser Asn Glu Ala Thr Glu Asn Arg Lys Thr Trp Trp
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	3045	3050	3055
	Glu Asn Asn Arg Arg Gln 3060	lle Trp His Ala 3065	a Met Leu Cys Gly Tyr Lys 3070
	Ile Ala Thr Ser Lys Val T 3075 308	hr Leu Asp Glu 30	ı Gly Trp Cys Gln Leu Pro 085
	Lys Asp Glu Glu Thr Asn 3090 3095	Gln Phe Leu / 310	Arg Trp Leu IIe Glu Trp Ala O
	Lys Gln Ala Cys Lys Glu 3105 3110	Lys Lys His Va 3115	I Ser Asp Ser Leu Lys Thr 3120
	3125	3130	
	3140	3145	g Lys Tyr IIe Ser Leu Asn 3150
	3155 31	60 3	u Asn IIe Lys Tyr Lys Gln 8165
	3170 3175	318	sp Asn Lys Pro Ser Glu Glu
	3185 3190	3195	o Ser Gln Cys Ala Leu Glu 3200 y Thr Lys Asn Asn Glu Asn
	3205	3210	3215 Leu Tyr Pro Gly Leu Tyr Phe
1-11	3220	3225	3230 al Leu Asp Gly Asn Ile Lys
	2025 20	40 3	3245
	3250 3255	326	la Leu Tyr Phe Phe Thr Pro 50 21 Phe Sor Thr His Arg Val
The Tall of	His Val Asp Ser Phe Tyr 3265 3270	3275	eu Phe Ser Thr His Arg Val
1	3285	3290	eu Lys Ser Ser IIe Ser Val 3295
	3300	3305	Leu His Phe Met Lys Lys 3310
The same	3315 33	20	Arg Ile Leu Asn Ile Pro Gln 3325 Por Lyg Asp Arg Tyr Ile Pro
	3330 3335	33	Ser Lys Asn Arg Tyr IIe Pro 40
M.	3345 3350	3355	nr Tyr IIe Tyr Met Glu Gly 3360 Met Tro Aso Lou Ser Ser Ser
	3365	3370	Met Trp Asp Leu Ser Ser Ser 3375
	3380	3385	lu Glu Leu Asp IIe Asn Asp 3390 3 Thr Leu IIe Clu Val Val
	3395 34	100	s Thr Leu IIe Glu Val Val 3405
	3410 3415	5. 34	
	3425 3430	3435	Asp Asp Glu Trp Asn Glu Leu 3440
	3445	3450	Pro Asn Thr Glu Pro Asn Asn 3455
	3460	3465	sn Thr Glu Pro Asn Thr Leu 3470 Sha lla lla Sar lla His Asp
			Phe IIe IIe Ser IIe His Asp 3485

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Arg Asp Leu Tyr Thr Gly Lys Glu lle Ser Tyr Asn lle Asn Met Ser
                                  3500
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     3490
  Thr Asn Thr Asn Asn Asp lie Pro Met Asn Ala Arg Asn Asp Ser Tyr
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                 3510
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  Arg Gly lie Asp Leu lie Asn Asp Ser Leu Val Val Leu Asn Leu Leu
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                        25
   Gly Asn Glu Gly Val Cys Met Pro Pro Arg Arg Lys Ser Ile Cys Ile
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   His Asn Leu Thr Leu Glu Glu Gln Thr Lys Asn Lys Tyr Gln Leu Arg
                   55
                                 60
   Glu Ala Phe lle Lys Cys Ala Ala Lys Glu Thr Asn Leu Leu Trp Asp
                               75
   Lys Tyr Lys Asn Asp Lys Asn Glu Ala Glu Glu Leu Leu Lys Lys Gly
                           90
                                         95
   Lys lie Pro Glu Asp Phe Met Arg lie Met Phe Tyr Thr Phe Gly Asp
                         105
           100
Phe Arg Asp Phe Cys Leu Glu Asn Asp Met Gly Lys Asp Val Asp Lys
                                      125
                       120
   Val Lys Lys Asn Ile Asn Lys Val Phe Asn Asn Ser Ser Lys Arg Gly
                    135
                                   140
Phe Lys Lys Ile Asp Pro Glu Asn Trp Trp Asn Glu Asn Gly Pro Gln
                                               160
                                 155
   lle Trp Asn Gly Met Leu Cys Ala Leu lle His Ala Asp Thr Lys Asp
N
                            170
              165
   Ser Ile Lys Asn Lys Asp Asn Tyr Lys Tyr Glu Lys Val Thr Ile Leu
                          185
                                        190
   Ala Lys Arg Asp Gly Ser Asn Gly Met Thr Leu Ser Glu Phe Ala Lys
                       200
                                      205
        195
   Lys Pro Lys Phe Leu Arg Trp Phe Val Glu Trp Tyr Asp Asp Tyr Cys
                                   220
                     215
   Lys Glu Arg Gln Lys Tyr Leu Thr Glu Val Ala Ser Thr Cys Lys Ser
                                 235
                                                240
                  230
   lle Asp Gly Gly Gln Leu Lys Cys Asp Arg Gly Cys Asn Asn Lys Cys
                            250
                                           255
   Asp Glu Tyr Lys Lys Tyr Met Arg Lys Lys Lys Glu Glu Trp Asn Leu
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                                 45
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Gln Asn Leu Cys Val His Tyr Leu Thr Lys Leu Asn Asp Asp Ser Lys
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Glu Glu Asp Leu Arg Glu Ala Phe Ile Lys Ser Ala Ala Ala Glu Thr
                            75
Phe Leu Leu Arg Gln Tyr Tyr Asn Ser Lys Asn Val Glu Asp Asp Lys
                                      95
                        90
lle Leu His Arg Asp Met Ile Pro Pro Glu Phe Phe Arg Ser Met Phe
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Tyr Thr Phe Gly Asp Tyr Arg Asp Ile Cys Leu Asp Thr Asp Ile Ser
                    120
                                   125
Glu Lys Ile Ala Asp His Asp Val Thr Thr Ala Lys Lys Lys Ile Thr
                 135
Ala Val Phe Gln Lys Ile Gly Ser Lys Thr Thr Asn Gly Lys Lys Val
               150
                             155
Leu Glu Arg Glu Gly Trp Trp Lys Glu Tyr Gly Leu Ser lle Trp Lys
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Gly Met Leu Cys Ala Leu Ser Tyr Asn Thr Glu Thr Lys Lys Met Asp
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Glu Gly Val Arg Thr Tyr Leu Met Lys Tyr lle Tyr Lys Asn Asn Asp
                    200
lle Lys Glu Tyr Leu Glu Glu Phe Ala Ser Arg Pro Pro Phe Leu Arg
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                                220
Trp Val Thr Glu Trp Gly Glu Asp Phe Val Lys Asn Arg Lys Lys Glu
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Leu Val Ser Leu Lys Lys Cys Asp Ser Cys Thr Leu Arg Asn Asn
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 Gly Thr Ser Asn Lys Thr Cys Asp Asp Asn Glu Asn Cys Gly Ala Cys
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 Lys Thr Gln Cys Glu Lys Tyr Lys Lys Trp Met Glu Arg Trp Lys Lys
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                    280
 His Tyr Ser Ser Gln Lys Lys Phe Gln Leu Tyr Lys Asn Ser Ala
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 Thr Tyr Asn Asn Gly Leu Ala Val Lys Glu Ala Asn Ser Glu Thr Tyr
                                             320
               310
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 Lys Asn Asp Pro Glu Val Thr Glu Ala Asn Ser Ala Lys His Ala Arg
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  Asn Gly Ala Cys Met Pro Pro Arg Arg Gln Lys Leu Cys Val Ser Gly
                                    45
  Leu Thr Lys Thr Asp Arg lie Lys Ala lie Glu Tyr lie Arg Thr Glu
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  Phe IIe Lys Ser Ala Ala IIe Glu Thr His Phe Ala Trp Asp Arg Tyr
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   Lys Glu Asp Asn Gly Glu Ala Glu Ala Glu Leu Lys Asn Gly Asn Ile
                                         95
                           90
   Pro Glu Gly Phe Lys Arg Gln Met Tyr Tyr Thr Phe Gly Asp Tyr Arg
          100
                         105
   Asp IIe Phe Phe Gly Arg Asp IIe Ser Thr His Ala Tyr IIe Ser Gly
                                     125
                      120
   Val Ser Pro Lys Val IIe Thr IIe Leu Glu Lys Glu Asn Asp Ala Lys
                                   140
                    135
   Tyr Ala Ala Lys Gln Asn Ser Asn Asn Glu Leu Leu Asp Asp Trp Trp
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                                155
   Asp Gln His Gly Lys Asp lle Trp Glu Gly Met Leu Cys Ala Leu Thr
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                            170
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   His Lys Ile Ser Asp Glu Glu Lys Lys Lys Glu Ile Lys Asn Lys Tyr
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   Ser Tyr Lys Lys Leu Asn Glu Ser Pro Lys Gly Ser Asn Lys Val Glu
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   Asp Phe Ala Lys Lys Pro Gln Phe Leu Arg Trp Phe Ile Glu Trp Gly
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   Asp Glu Phe Cys Ala Gln Arg Glu Glu Lys Glu Ala Lys Val Lys Val
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   Ser Cys Ser Asp Ala Lys Asp Tyr Asp Gly Cys Lys Asn Thr Lys Ser
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   Asn Ala Ser Cys Val Ser Ala Cys Lys Val Tyr Glu Asp Tyr lle Thr
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                          265
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   Lys Lys Lys Val Glu Tyr Thr Lys Gln Lys Gly Lys Phe Asp Ala Glu
                       280
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Ala Cys Met Pro Pro Arg Arg Gln Lys Leu Cys Val Arg Asp Leu Thr 35 40 45
Gln Gly Gly Glu Ile Arg Lys Pro Glu Asp Ile Leu Thr Lys Phe Ile 50 55 60
Asn Cys Ala Ala Lys Glu Thr His Phe Ala Trp His Lys Tyr Lys Lys 65 70 75 80
Asp Asn Val Asn Ala Glu Asn Glu Leu Lys Ser Gly Lys Ile Pro Glu 85 90 95
Gly Phe Arg Lys Gln Met Tyr Tyr Thr Phe Gly Asp Phe Arg Asp Ile 100 105 110
Phe Phe Gly Thr Asp IIe Ser Ser Cys Arg Tyr IIe Lys Asp Thr Ser 115 120 125
Gln Thr IIe Lys Ser Lys Leu Gly Asp Gln Ala Thr Thr Glu Lys Gly 130 135 140
Asp Thr His IIe Asp Asp Asn Lys Lys Leu Gln Glu Trp Trp Thr IIe 145 150 155 160
His Gly Pro Lys IIe Trp Glu Gly Met Leu Cys Ala Leu Thr Asn Gly 165 170 175
Leu Ser Glu Ser Glu Lys Lys Asn Ile Leu Gln Asp Tyr Ser Tyr Asn 180 185 190
Lys Leu Asn Asn Ala Glu Lys Asp Asp Cys Cys Leu Glu Lys Phe Ala 195 200 205
Ser Lys Pro Gln Phe Leu Arg Trp Tyr Val Glu Trp Ser Asp Glu Phe 210 215 220
Cys Arg Glu Arg Lys Lys Leu Glu Asp Lys Val Glu Asp Val Cys Ile 225 230 235 240
Lys Ala Lys Asp Tyr Glu Gly Cys Lys Asn Asn Lys Ser Asn Asn Ser 245 250 255
Cys Val Lys Val Cys Lys Glu Tyr Glu Asn Tyr Ile Thr Gly Lys Lys 260 265 270
Thr Gln Tyr Glu Ser Gln Glu Gly Lys Phe Asn Thr Glu Lys Arg Gln 275 280 285
Lys Lys Pro Glu Tyr Asn Ser Tyr Ser Lys Lys Asp Ala Ser Glu Tyr 290 295 300
Leu Lys Asp Lys 305